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P#22

## RAW SEQUENCE LISTING

DATE: 09/26/2002

PATENT APPLICATION: US/09/543,371A

TIME: 16:28:03

Input Set : A:\09543371.ST25.txt

Output Set: N:\CRF4\09262002\I543371A.raw

3 <110> APPLICANT: Kalluri, Raghuram  
 5 <120> TITLE OF INVENTION: Anti-Angiogenic Proteins and Fragments and Methods of Use  
 Thereof

7 &lt;130&gt; FILE REFERENCE: 02312/2085B (formerly 1440.1027-005)

9 &lt;140&gt; CURRENT APPLICATION NUMBER: US 09/543,371A

10 &lt;141&gt; CURRENT FILING DATE: 2000-04-04

12 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/089,689

13 &lt;151&gt; PRIOR FILING DATE: 1998-06-17

15 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/126,175

16 &lt;151&gt; PRIOR FILING DATE: 1999-03-25

18 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/335,224

19 &lt;151&gt; PRIOR FILING DATE: 1999-06-17

21 &lt;160&gt; NUMBER OF SEQ ID NOS: 18

23 &lt;170&gt; SOFTWARE: PatentIn version 3.1

25 &lt;210&gt; SEQ ID NO: 1

26 &lt;211&gt; LENGTH: 690

27 &lt;212&gt; TYPE: DNA

28 &lt;213&gt; ORGANISM: Homo sapiens

30 &lt;220&gt; FEATURE:

31 &lt;221&gt; NAME/KEY: CDS

32 &lt;222&gt; LOCATION: (1)..(687)

33 &lt;223&gt; OTHER INFORMATION:

35 &lt;400&gt; SEQUENCE: 1

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37 Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp

38 1 5 10 15

40 gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct 96

41 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser

42 20 25 30

44 ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc 144

45 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly

46 35 40 45

48 acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc 192

49 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe

50 50 55 60

52 tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg 240

53 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser

54 65 70 75 80

56 tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc 288

57 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile

58 85 90 95

60 acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag 336

61 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu

62 100 105 110

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64 gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca      384
65 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
66      115      120      125
68 ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt gtg      432
69 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
70      130      135      140
72 atg cac acc agc gct ggt gca gaa ggc tct ggc caa gcc ctg gcg tcc      480
73 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
74 145      150      155      160
76 ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag tgt      528
77 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
78      165      170      175
80 cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg      576
81 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
82      180      185      190
84 ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc      624
85 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
86      195      200      205
88 acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa gtc      672
89 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
90      210      215      220
92 tgt atg aga aga aca taa      690
93 Cys Met Arg Arg Thr
94 225
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 229
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
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105 1      5      10      15
108 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
109      20      25      30
112 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
113      35      40      45
116 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
117      50      55      60
120 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
121 65      70      75      80
124 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
125      85      90      95
128 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
129      100      105      110
132 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
133      115      120      125
136 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
137      130      135      140
140 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
141 145      150      155      160

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144 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
145                               165                               170                               175
148 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
149                               180                               185                               190
152 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
153                               195                               200                               205
156 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
157       210                               215                               220
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161 225
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166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for Arresten
172 <400> SEQUENCE: 3
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177 <211> LENGTH: 27
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: pET22b(+) reverse oligonuceotide primer for Arresten
184 <400> SEQUENCE: 4
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189 <211> LENGTH: 684
190 <212> TYPE: DNA
191 <213> ORGANISM: Homo sapiens
193 <220> FEATURE:
194 <221> NAME/KEY: CDS
195 <222> LOCATION: (1)..(681)
196 <223> OTHER INFORMATION:
198 <400> SEQUENCE: 5
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200 Val Ser Ile Gly Tyr Leu Leu Val Lys His Ser Gln Thr Asp Gln Glu
201 1                               5                               10                               15
203 ccc atg tgc ccg gtg ggc atg aac aaa ctc tgg agt gga tac agc ctg                               96
204 Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
205       20                               25                               30
207 ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg                               144
208 Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
209       35                               40                               45
211 gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc                               192
212 Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
213       50                               55                               60
215 aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac                               240
216 Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr

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217 65          70          75          80
219 tgg ctc tct acc act gcg ccg ctg ccc atg atg ccc gtg gcc gag gac      288
220 Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
221          85          90          95
223 gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc      336
224 Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
225          100          105          110
227 atc gcc atc gcg gtc cac agt cag gat gtc tcc atc cca cac tgc cca      384
228 Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
229          115          120          125
231 gct ggg tgg cgg agt ttg tgg atc gga tat tcc ttc ctc atg cac acg      432
232 Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
233          130          135          140
235 gcg gcg gga gac gaa ggc ggt ggc caa tca ctg gtg tca ccg ggc agc      480
236 Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
237 145          150          155          160
239 tgt cta gag gac ttc cgc gcc aca cca ttc atc gaa tgc aat gga ggc      528
240 Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
241          165          170          175
243 cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc      576
244 Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
245          180          185          190
247 acc att ccc gag cag agc ttc cag ggc tcg ccc tcc gcc gac acg ctc      624
248 Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
249          195          200          205
251 aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg      672
252 Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
253          210          215          220
255 aag aac ctg tga      684
256 Lys Asn Leu
257 225
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 227
262 <212> TYPE: PRT
263 <213> ORGANISM: Homo sapiens
265 <400> SEQUENCE: 6
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271 Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
272          20          25          30
275 Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
276          35          40          45
279 Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
280          50          55          60
283 Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
284 65          70          75          80
287 Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
288          85          90          95
291 Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala

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292          100          105          110
295 Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
296          115          120          125
299 Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
300          130          135          140
303 Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
304 145          150          155          160
307 Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
308          165          170          175
311 Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
312          180          185          190
315 Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
316          195          200          205
319 Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
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323 Lys Asn Leu
324 225
327 <210> SEQ ID NO: 7
328 <211> LENGTH: 27
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for Canstatin
335 <400> SEQUENCE: 7
336 cgggacccctg tcagcatcgg ctacctc 27
339 <210> SEQ ID NO: 8
340 <211> LENGTH: 27
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: pET22b(+) reverse oligonucleotide primer for Canstatin
347 <400> SEQUENCE: 8
348 cccaagcttc aggttcttca tgcacac 27
351 <210> SEQ ID NO: 9
352 <211> LENGTH: 735
353 <212> TYPE: DNA
354 <213> ORGANISM: Homo sapiens
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358 <222> LOCATION: (1)..(732)
359 <223> OTHER INFORMATION:
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363 <222> LOCATION: (160)..(732)
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368 <221> NAME/KEY: misc_feature
369 <222> LOCATION: (1)..(372)
370 <223> OTHER INFORMATION: Tumstatin 333

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VERIFICATION SUMMARY

DATE: 09/26/2002

PATENT APPLICATION: US/09/543,371A

TIME: 16:28:04

Input Set : A:\09543371.ST25.txt

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